

SEQUENCE LISTING

<110> YIP, CECIL

<120> IDENTIFICATION OF COMPOUNDS FOR MODULATING DIMERIC RECEPTORS

<130> P04885US1

<140> 09/744628

<141> 2000-05-25

<150> PCT/CA00/00605

<151> 2000-05-25

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 30

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) .. (30)

<223> X(1)=N,Q,T,Y X(2)=K,R X(3)=A,L,I,P,F,W,M,C,G
X(4)=D X(5)=Q,S,T,N X(6)=A,V,I,P,F,W,M,C,G
X(7)=D X(8)=K,H X(9)=A,V,I,P,L,W,M,C,G
X(10)=A,V,I,P,L,W,M,C,G X(11)=Q,S,T,N X(12)=H,R

<400> 1

Phe	Val	Asn	Gln	His	Leu	Cys	Gly	Xaa	Xaa	Leu	Xaa	Xaa	Ala	Leu	Xaa
1				5				10					15		

Xaa	Val	Cys	Gly	Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Thr	Pro	Xaa	Thr
		20					25					30	

<210> 2

<211> 21

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) .. (21)

<223> X(1)=D X(2)=Q,S,T,Y
X(3)=N,Q,S,T,Y X(4)=,Q,S,T,Y
X(5)=D X(6)=Q,S,T,Y

<400> 2

Gly	Ile	Val	Xaa	Xaa	Cys	Cys	Xaa	Ser	Ile	Cys	Ser	Leu	Tyr	Xaa	Leu
1				5				10					15		

Xaa Asn Tyr Cys Xaa

20

<210> 3
 <211> 30
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) .. (30)
 <223> X(1)=N,Q,T,Y X(2)=K,R X(3)=A,L,I,P,F,W,M,C,G X(4)=D
 X(5)=Q,S,T,N X(6)=A,V,I,P,F,W,M,C,G X(7)=D X(8)=K,H
 X(9)=A,V,I,P,L,W,M,C,G X(10)=A,V,I,P,L,W,M,C,G X(11)=Q,S,T,N
 X(12)=H,R X(13)=H,R

<400> 3

Phe Val Asn Gln His Leu Cys Gly Xaa Xaa Leu Xaa Xaa Ala Leu Xaa
 1 5 10 15

Xaa Val Cys Gly Xaa Xaa Gly Xaa Xaa Xaa Thr Xaa Pro Thr
 20 25 30

<210> 4
 <211> 21
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) .. (21)
 <223> X(1)=D X(2)=Q,S,T,Y
 X(3)=N,Q,S,T,Y X(4)=Q,S,T,Y
 X(5)=D X(6)=Q,S,T,Y

<400> 4

Gly Ile Val Xaa Xaa Cys Cys Xaa Ser Ile Cys Ser Leu Tyr Xaa Leu
 1 5 10 15

Xaa Asn Tyr Cys Xaa
 20

<210> 5
 <211> 30
 <212> PRT
 <213> Bos taurus

<220>
 <221> PEPTIDE
 <222> (1) .. (30)
 <223> X(1)=N,Q,T,Y X(2)=K,R X(3)=A,L,I,P,F,W,M,C,G
 X(4)=D X(5)=Q,S,T,N X(6)=A,V,I,P,F,W,M,C,G
 X(7)=D X(8)=K,H X(9)=A,V,I,P,L,W,M,C,G
 X(10)=A,V,I,P,L,W,M,C,G X(11)=Q,S,T,N X(12)=H,R

<400> 5

Phe Val Asn Gln His Leu Cys Gly Xaa Xaa Leu Xaa Xaa Ala Leu Xaa
 1 5 10 15

Xaa Val Cys Gly Xaa Xaa Gly Xaa Xaa Xaa Thr Pro Xaa Ala
 20 25 30

<210> 6

<211> 21

<212> PRT

<213> Bos taurus

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> X(1)=D X(2)=Q,S,T,Y
 X(3)=N,Q,S,T,Y X(4)=Q,S,T,Y
 X(5)=D X(6)=Q,S,T,Y

<400> 6

Gly Ile Val Xaa Xaa Cys Cys Xaa Ser Val Cys Ser Leu Tyr Xaa Leu
 1 5 10 15

Xaa Asn Tyr Cys Xaa
 20

<210> 7

<211> 30

<212> PRT

<213> Sus scrofa

<220>

<221> PEPTIDE

<222> (1)..(30)

<223> X(1)=N,Q,T,Y X(2)=K,R X(3)=A,L,I,P,F,W,M,C,G
 X(4)=D X(5)=Q,S,T,N X(6)=A,V,I,P,F,W,M,C,G
 X(7)=D X(8)=K,H X(9)=A,V,I,P,L,W,M,C,G
 X(10)=A,V,I,P,L,W,M,C,G X(11)=Q,S,T,N X(12)=H,R

<400> 7

Phe Val Asn Gln His Leu Cys Gly Xaa Xaa Leu Xaa Xaa Ala Leu Xaa
 1 5 10 15

Xaa Val Cys Gly Xaa Xaa Gly Xaa Xaa Xaa Thr Pro Xaa Ala
 20 25 30

<210> 8

<211> 21

<212> PRT

<213> Sus scrofa

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> X(1)=D X(2)=Q,S,T,Y
 X(3)=N,Q,S,T,Y X(4)=Q,S,T,Y
 X(5)=D X(6)=Q,S,T,Y

<400> 8

Gly Ile Val Xaa Xaa Cys Cys Xaa Ser Ile Cys Ser Leu Tyr Xaa Leu
 1 5 10 15

Xaa Asn Tyr Cys Xaa
 20

<210> 9
 <211> 30
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)..(30)

<400> 9

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
 1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
 20 25 30

<210> 10
 <211> 21
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)..(21)

<400> 10

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
 1 5 10 15

Glu Asn Tyr Cys Asn
 20

<210> 11
 <211> 30
 <212> PRT
 <213> Bos taurus

<220>
 <221> PEPTIDE
 <222> (1)..(30)

<400> 11

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr

1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Ala
20 25 30

<210> 12
<211> 21
<212> PRT
<213> Bos taurus

<220>
<221> PEPTIDE
<222> (1)..(21)

<400> 12

Gly Ile Val Glu Gln Cys Cys Ala Ser Val Cys Ser Leu Tyr Gln Leu
1 5 10 15

Glu Asn Tyr Cys Asn
20

<210> 13
<211> 30
<212> PRT
<213> Sus scrofa

<220>
<221> PEPTIDE
<222> (1)..(30)

<400> 13

Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu Tyr
1 5 10 15

Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Ala
20 25 30

<210> 14
<211> 21
<212> PRT
<213> Sus scrofa

<220>
<221> PEPTIDE
<222> (1)..(21)

<400> 14

Gly Ile Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu
1 5 10 15

Glu Asn Tyr Cys Asn
20

<210> 15
<211> 27
<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(27)

<400> 15

Met Gly Thr Gly Gly Arg Arg Gly Ala Ala Ala Ala Pro Leu Leu Val
1 5 10 15

Ala Val Ala Ala Leu Leu Leu Gly Ala Ala Gly
20 25

<210> 16

<211> 719

<212> PRT

<213> Homo sapiens

<220>

<221> CHAIN

<222> (1)..(719)

<400> 16

His Leu Tyr Pro Gly Glu Val Cys Pro Gly Met Asp Ile Arg Asn Asn
1 5 10 15

Leu Thr Arg Leu His Glu Leu Glu Asn Cys Ser Val Ile Glu Gly His
20 25 30

Leu Gln Ile Leu Leu Met Phe Lys Thr Arg Pro Glu Asp Phe Arg Asp
35 40 45

Leu Ser Phe Pro Lys Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe
50 55 60

Arg Val Tyr Gly Leu Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr
65 70 75 80

Val Ile Arg Gly Ser Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe
85 90 95

Glu Met Val His Leu Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile
100 105 110

Thr Arg Gly Ser Val Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu
115 120 125

Ala Thr Ile Asp Trp Ser Arg Ile Leu Asp Ser Val Glu Asp Asn His
130 135 140

Ile Val Leu Asn Lys Asp Asp Asn Glu Glu Cys Gly Asp Ile Cys Pro
145 150 155 160

Gly Thr Ala Lys Gly Lys Thr Asn Cys Pro Ala Thr Val Ile Asn Gly
165 170 175

Gln Phe Val Glu Arg Cys Trp Thr His Ser His Cys Gln Lys Val Cys

				180					185					190		
Pro	Thr	Ile	Cys	Lys	Ser	His	Gly	Cys	Thr	Ala	Glu	Gly	Leu	Cys	Cys	
		195					200					205				
His	Ser	Glu	Cys	Leu	Gly	Asn	Cys	Ser	Gln	Pro	Asp	Asp	Pro	Thr	Lys	
	210					215					220					
Cys	Val	Ala	Cys	Arg	Asn	Phe	Tyr	Leu	Asp	Gly	Arg	Cys	Val	Glu	Thr	
225					230					235					240	
Cys	Pro	Pro	Pro	Tyr	Tyr	His	Phe	Gln	Asp	Trp	Arg	Cys	Val	Asn	Phe	
				245					250					255		
Ser	Phe	Cys	Gln	Asp	Leu	His	His	Lys	Cys	Lys	Asn	Ser	Arg	Arg	Gln	
			260					265					270			
Gly	Cys	His	Gln	Tyr	Val	Ile	His	Asn	Asn	Lys	Cys	Ile	Pro	Glu	Cys	
		275					280					285				
Pro	Ser	Gly	Tyr	Thr	Met	Asn	Ser	Ser	Asn	Leu	Leu	Cys	Thr	Pro	Cys	
	290					295					300					
Leu	Gly	Pro	Cys	Pro	Lys	Val	Cys	His	Leu	Leu	Glu	Gly	Glu	Lys	Thr	
305					310					315					320	
Ile	Asp	Ser	Val	Thr	Ser	Ala	Gln	Glu	Leu	Arg	Gly	Cys	Thr	Val	Ile	
				325					330					335		
Asn	Gly	Ser	Leu	Ile	Ile	Asn	Ile	Arg	Gly	Gly	Asn	Asn	Leu	Ala	Ala	
			340					345					350			
Glu	Leu	Glu	Ala	Asn	Leu	Gly	Leu	Ile	Glu	Glu	Ile	Ser	Gly	Tyr	Leu	
		355					360					365				
Lys	Ile	Arg	Arg	Ser	Tyr	Ala	Leu	Val	Ser	Leu	Ser	Phe	Phe	Arg	Lys	
	370					375					380					
Leu	Arg	Leu	Ile	Arg	Gly	Glu	Thr	Leu	Glu	Ile	Gly	Asn	Tyr	Ser	Phe	
385					390					395					400	
Tyr	Ala	Leu	Asp	Asn	Gln	Asn	Leu	Arg	Gln	Leu	Trp	Asp	Trp	Ser	Lys	
				405					410					415		
His	Asn	Leu	Thr	Thr	Thr	Gln	Gly	Lys	Leu	Phe	Phe	His	Tyr	Asn	Pro	
			420					425					430			
Lys	Leu	Cys	Leu	Ser	Glu	Ile	His	Lys	Met	Glu	Glu	Val	Ser	Gly	Thr	
		435					440					445				
Lys	Gly	Arg	Gln	Glu	Arg	Asn	Asp	Ile	Ala	Leu	Lys	Thr	Asn	Gly	Asp	
	450					455						460				
Lys	Ala	Ser	Cys	Glu	Asn	Glu	Leu	Leu	Lys	Phe	Ser	Tyr	Ile	Arg	Thr	
465					470					475					480	
Ser	Phe	Asp	Lys	Ile	Leu	Leu	Arg	Trp	Glu	Pro	Tyr	Trp	Pro	Pro	Asp	
				485					490					495		

Phe Arg Asp Leu Leu Gly Phe Met Leu Phe Tyr Lys Glu Ala Pro Tyr
 500 505 510
 Gln Asn Val Thr Glu Phe Asp Gly Gln Asp Ala Cys Gly Ser Asn Ser
 515 520 525
 Trp Thr Val Val Asp Ile Asp Pro Pro Leu Arg Ser Asn Asp Pro Lys
 530 535 540
 Ser Gln Asn His Pro Gly Trp Leu Met Arg Gly Leu Lys Pro Trp Thr
 545 550 555 560
 Gln Tyr Ala Ile Phe Val Lys Thr Leu Val Thr Phe Ser Asp Glu Arg
 565 570 575
 Arg Thr Tyr Gly Ala Lys Ser Asp Ile Ile Tyr Val Gln Thr Asp Ala
 580 585 590
 Thr Asn Pro Ser Val Pro Leu Asp Pro Ile Ser Val Ser Asn Ser Ser
 595 600 605
 Ser Gln Ile Ile Leu Lys Trp Lys Pro Pro Ser Asp Pro Asn Gly Asn
 610 615 620
 Ile Thr His Tyr Leu Val Phe Trp Glu Arg Gln Ala Glu Asp Ser Glu
 625 630 635 640
 Leu Phe Glu Leu Asp Tyr Cys Leu Lys Gly Leu Lys Leu Pro Ser Arg
 645 650 655
 Thr Trp Ser Pro Pro Phe Glu Ser Glu Asp Ser Gln Lys His Asn Gln
 660 665 670
 Ser Glu Tyr Glu Asp Ser Ala Gly Glu Cys Cys Ser Cys Pro Lys Thr
 675 680 685
 Asp Ser Gln Ile Leu Lys Glu Leu Glu Glu Ser Ser Phe Arg Lys Thr
 690 695 700
 Phe Glu Asp Tyr Leu His Asn Val Val Phe Val Pro Arg Pro Ser
 705 710 715

<210> 17
 <211> 620
 <212> PRT
 <213> Homo sapiens

<220>
 <221> CHAIN
 <222> (1)..(620)

<400> 17

Ser Leu Gly Asp Val Gly Asn Val Thr Val Ala Val Pro Thr Val Ala
 1 5 10 15
 Ala Phe Pro Asn Thr Ser Ser Thr Ser Val Pro Thr Ser Pro Glu Glu
 20 25 30

His Arg Pro Phe Glu Lys Val Val Asn Lys Glu Ser Leu Val Ile Ser
 35 40 45
 Gly Leu Arg His Phe Thr Gly Tyr Arg Ile Glu Leu Gln Ala Cys Asn
 50 55 60
 Gln Asp Thr Pro Glu Glu Arg Cys Ser Val Ala Ala Tyr Val Ser Ala
 65 70 75 80
 Arg Thr Met Pro Glu Ala Lys Ala Asp Asp Ile Val Gly Pro Val Thr
 85 90 95
 His Glu Ile Phe Glu Asn Asn Val Val His Leu Met Trp Gln Glu Pro
 100 105 110
 Lys Glu Pro Asn Gly Leu Ile Val Leu Tyr Glu Val Ser Tyr Arg Arg
 115 120 125
 Tyr Gly Asp Glu Glu Leu His Leu Cys Val Ser Arg Lys His Phe Ala
 130 135 140
 Leu Glu Arg Gly Cys Arg Leu Arg Gly Leu Ser Pro Gly Asn Tyr Ser
 145 150 155 160
 Val Arg Ile Arg Ala Thr Ser Leu Ala Gly Asn Gly Ser Trp Thr Glu
 165 170 175
 Pro Thr Tyr Phe Tyr Val Thr Asp Tyr Leu Asp Val Pro Ser Asn Ile
 180 185 190
 Ala Lys Ile Ile Ile Gly Pro Leu Ile Phe Val Phe Leu Phe Ser Val
 195 200 205
 Val Ile Gly Ser Ile Tyr Leu Phe Leu Arg Lys Arg Gln Pro Asp Gly
 210 215 220
 Pro Leu Gly Pro Leu Tyr Ala Ser Ser Asn Pro Glu Tyr Leu Ser Ala
 225 230 235 240
 Ser Asp Val Phe Pro Cys Ser Val Tyr Val Pro Asp Glu Trp Glu Val
 245 250 255
 Ser Arg Glu Lys Ile Thr Leu Leu Arg Glu Leu Gly Gln Gly Ser Phe
 260 265 270
 Gly Met Val Tyr Glu Gly Asn Ala Arg Asp Ile Ile Lys Gly Glu Ala
 275 280 285
 Glu Thr Arg Val Ala Val Lys Thr Val Asn Glu Ser Ala Ser Leu Arg
 290 295 300
 Glu Arg Ile Glu Phe Leu Asn Glu Ala Ser Val Met Lys Gly Phe Thr
 305 310 315 320
 Cys His His Val Val Arg Leu Leu Gly Val Val Ser Lys Gly Gln Pro
 325 330 335
 Thr Leu Val Val Met Glu Leu Met Ala His Gly Asp Leu Lys Ser Tyr
 340 345 350

Leu Arg Ser Leu Arg Pro Glu Ala Glu Asn Asn Pro Gly Arg Pro Pro
 355 360 365
 Pro Thr Leu Gln Glu Met Ile Gln Met Ala Ala Glu Ile Ala Asp Gly
 370 375 380
 Met Ala Tyr Leu Asn Ala Lys Lys Phe Val His Arg Asp Leu Ala Ala
 385 390 395 400
 Arg Asn Cys Met Val Ala His Asp Phe Thr Val Lys Ile Gly Asp Phe
 405 410 415
 Gly Met Thr Arg Asp Ile Tyr Glu Thr Asp Tyr Tyr Arg Lys Gly Gly
 420 425 430
 Lys Gly Leu Leu Pro Val Arg Trp Met Ala Pro Glu Ser Leu Lys Asp
 435 440 445
 Gly Val Phe Thr Thr Ser Ser Asp Met Trp Ser Phe Gly Val Val Leu
 450 455 460
 Trp Glu Ile Thr Ser Leu Ala Glu Gln Pro Tyr Gln Gly Leu Ser Asn
 465 470 475 480
 Glu Gln Val Leu Lys Phe Val Met Asp Gly Gly Tyr Leu Asp Gln Pro
 485 490 495
 Asp Asn Cys Pro Glu Arg Val Thr Asp Leu Met Arg Met Cys Trp Gln
 500 505 510
 Phe Asn Pro Lys Met Arg Pro Thr Phe Leu Glu Ile Val Asn Leu Leu
 515 520 525
 Lys Asp Asp Leu His Pro Ser Phe Pro Glu Val Ser Phe Phe His Ser
 530 535 540
 Glu Glu Asn Lys Ala Pro Glu Ser Glu Glu Leu Glu Met Glu Phe Glu
 545 550 555 560
 Asp Met Glu Asn Val Pro Leu Asp Arg Ser Ser His Cys Gln Arg Glu
 565 570 575
 Glu Ala Gly Gly Arg Asp Gly Gly Ser Ser Leu Gly Phe Lys Arg Ser
 580 585 590
 Tyr Glu Glu His Ile Pro Tyr Thr His Met Asn Gly Gly Lys Lys Asn
 595 600 605
 Gly Arg Ile Leu Thr Leu Pro Arg Ser Asn Pro Ser
 610 615 620